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Db      61 YQ--MEHPDEHQNVROLIGKHERQONVPEVLIDREKLAAMDRLLELVEDEFAMILE 117
Qy      125 DTPEFVARLLIREAKAYLDSLPPPEFKALTHYAADSGYSMHCPGSGVAFLKSPYGMF 184
Db      118 DTDDEFIAGRAVAAMTRRYQOOLPPLFSALMKISDIHEYSAAPHOGSGVGTFTKTPAGRFY 177
Qy      185 HOFEGENMLRADVCNAVDELQGLLDHTGPAASERNARLYNCDELHYVNTGSTSTNKIV 244
Db      178 HDVYGENLPRTDMGIERSTGLSLDHTGAFGESEKVAARVFGADRSWSVVGTSNRTI 237
Qy      245 WNSTVAPGDIYVDRNCHKSVLHSIIMTGAVPVFLMPTNHHGIIIGPIKSEFAMENIOK 304
Db      238 MQACMDNDVVVDRNCHKSIIEOGLMLTGAKPVYVWPSNRKYGIIIGPIYQEQMPELTK 297
Qy      305 KIARNPATDK-NAKPRVLTITOSTYDGVLYNVEIEKMLDGKIDTLHFDEAMLPATPH 363
Db      298 KISSPLTKDAGOKPSYCVVNTCTYDGCYNAAEADLLEKTSDBRLHFDAMYGARFN 357
Qy      364 DFYGDYHAIAGDRPRCKESWVSTOSTHKLGLAGLSQASOILVODADQNRDLRDVFEAYL 423
Db      358 PIYADHYARNGEPDNGPTVFATHSTHKLNLALSOASYIHVREG-RGAINFSRFQAYM 416
Qy      424 MHTSTPOYSIIASCVAAMAEAPGCTALVEESLKEALDPRARKVDEWGTD--WVF 481
Db      417 MHATTSPLYAICASNDVAVSMNDGNSGLSTOEVIDEAVDFRQAMARLYKEFTADGSMWF 476
Qy      482 KVM-----GPTDLSBDGLEBRDAMMLKANERWGHGFLAEGFNMLDP 523
Db      477 KPMKEVVTDPQTKTYDFADAPTKL--TTVQDCVWVHGPESMNGFKDIPDNMSGLDP 533
Qy      524 IKATITTPGLDVEGDFSDFGIPALVITYKLAEGVIVETGLYSFFIMFTIGITKGRN 583
Db      534 IKVSIILAPGMEGDEL-BETGVPAALVTAMLGRGIVPRTTDFQIMPLFSMGVTRGKM 592
Qy      584 TMVAALQOPRDYDKQPLMKVLPFVQKHP-RYEVNGKDLCTQIHEVYKANDVARTT 642
Db      593 TLVNTLCSFKRHAYANPLAQPVELVEQPYTYANNGIHDLGDTMAKLENNPGARLN 652
Qy      643 EMTLSDMVPAMKPTDAFSKMAHRIKIERVAIDLEGRTAVALLTPYPGIPLLIPGERF-- 700
Db      653 EAYSGLPVAEITPREXNAIYVNNVELVISIENLPGRIANSVIIRPGIIPMLLSGENFGD 712
Qy      701 -NKVIYNYLKFAREFNEKPPGFTDNHGLVKQIVDGAAYVYDVCV 745
Db      713 KNSPQVSYLRSLQSMWHFPGFEHETEG--TEIIDG--IYHWCVK 754

RESULT 13
ID      06XJ52 PRELIMINARY; PRT; 756 AA.
AC      06XJ52;
DT      05-JUL-2004 (TReMBLrel. 27, Created)
DT      05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE      05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE      Arginine decarboxylase.
GN      Name=adi;
OS      Shigella boydii.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Shigella.
CX      NCBI_TaxID=621;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CDPH;
RA      Chan Y.C., Blaschek H.P.,
RL      Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.
DR      EMBL, AY231474; AAF59882.1;
DR      GO; GO:0005737; C:cytoplasm; IEA.
DR      GO; GO:0016831; F:carboxy-lyase activity; IEA.
DR      GO; GO:0003824; F:catalytic activity; IEA.
DR      GO; GO:0006520; P:amino acid metabolism; IEA.
DR      InterPro; IPR01006; CheY like.
DR      InterPro; IPR000310; Decarboxylase.
DR      InterPro; IPR008286; Decarboxylase_C.

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DR      InterPro; IPR005308; OKR_DC_1_N.
DR      InterPro; IPR011193; Orn_decarb.
DR      Pfam; PF01276; OKR_DC_1; 1.
DR      Pfam; PF03711; OKR_DC_1_C; 1.
DR      Pfam; PF03709; OKR_DC_1_N; 1.
DR      Pfam; F1RSP00393; Orn_decarb; 1.
DR      PROSITE; PS00703; OKR_DC_1; 1.
SQ      SEQUENCE 756 AA; 84690 MW; C26B2B3B3CAA71F CRC64;

Query Match      34.8%; Score 1377.5; DB 2; Length 756;
Best Local Similarity 37.1%; Pred No. 9.2e-87;
Matches 284; Conservative 157; Mismatches 284; Indels 41; Gaps 14;

Qy      7 VIIDEDPFSNS-SGLGIRYLAKAIEDEGLEVLGVTSGYDLYSFAQOGRASAPFLSID 65
Db      4 VLIYSEFLHDTWGNVAVERLADLSQONTVIVKSTFDD--GFAILSNBAIDCLMPS 61
Qy      66 DEEIVEKEPEALIQLNFOEIRYNEEIPITLHGE-TYTSNHPNDVARELHGFIHME 124
Db      62 YQ--MEHPDEHQNVROLIGKHERQONVPEVLIDREKLAAMDRLLELVEDEFAMILE 118
Qy      125 DTPEFVARLLIREAKAYLDSLPPPEFKALTHYAADSGYSMHCPGSGVAFLKSPYGMF 184
Db      119 DTDDEFIAGRAVAAMTRRYQOOLPPLFSALMKISDIHEYSAAPHOGSGVGTFTKTPAGRFY 178
Qy      185 HOFEGENMLRADVCNAVDELQGLLDHTGPAASERNARLYNCDELHYVNTGSTSTNKIV 244
Db      179 HDVYGENLPRTDMGIERSTGLSLDHTGAFGESEKVAARVFGADRSWSVVGTSNRTI 238
Qy      245 WNSTVAPGDIYVDRNCHKSVLHSIIMTGAVPVFLMPTNHHGIIIGPIKSEFAMENIOK 304
Db      239 MQACMDNDVVVDRNCHKSIIEOGLMLTGAKPVYVWPSNRKYGIIIGPIYQEQMPELTK 298
Qy      305 KIARNPATDK-NAKPRVLTITOSTYDGVLYNVEIEKMLDGKIDTLHFDEAMLPATPH 363
Db      299 KISESLTKDAGOKPSYCVVNTCTYDGCYNAAEADLLEKTSDBRLHFDAMYGARFN 358
Qy      364 DFYGDYHAIAGDRPRCKESWVSTOSTHKLGLAGLSQASOILVODADQNRDLRDVFEAYL 423
Db      359 PIYADHYARNGEPDNGPTVFATHSTHKLNLALSOASYIHVREG-RGAINFSRFQAYM 417
Qy      424 MHTSTPOYSIIASCVAAMAEAPGCTALVEESLKEALDPRARKVDEWGTD--WVF 481
Db      418 MHATTSPLYAICASNDVAVSMNDGNSGLSTOEVIDEAVDFRQAMARLYKEFTADGSMWF 477
Qy      482 KVM-----GPTDLSBDGLEBRDAMMLKANERWGHGFLAEGFNMLDP 523
Db      478 KPMKEVVTDPQTKTYDFADAPTKL--TTVQDCVWVHGPESMNGFKDIPDNMSGLDP 534
Qy      524 IKATITTPGLDVEGDFSDFGIPALVITYKLAEGVIVETGLYSFFIMFTIGITKGRN 583
Db      535 IKVSIILAPGMEGDEL-BETGVPAALVTAMLGRGIVPRTTDFQIMPLFSMGVTRGKM 593
Qy      584 TMVAALQOPRDYDKQPLMKVLPFVQKHP-RYEVNGKDLCTQIHEVYKANDVARTT 642
Db      594 TLVNTLCSFKRHAYANPLAQPVELVEQPYTYANNGIHDLGDTMAKLENNPGARLN 653
Qy      643 EMTLSDMVPAMKPTDAFSKMAHRIKIERVAIDLEGRTAVALLTPYPGIPLLIPGERF-- 700
Db      654 EAYSGLPVAEITPREXNAIYVNNVELVISIENLPGRIANSVIIRPGIIPMLLSGENFGD 713
Qy      701 -NKVIYNYLKFAREFNEKPPGFTDNHGLVKQIVDGAAYVYDVCV 745
Db      714 KNSPQVSYLRSLQSMWHFPGFEHETEG--TEIIDG--IYHWCVK 755

RESULT 14
ID      08Z1P1 PRELIMINARY; PRT; 756 AA.
AC      08Z1P1; Q7C5L6;
DT      01-MAR-2002 (TReMBLrel. 20, Created)
DT      01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT      25-OCT-2004 (TReMBLrel. 28, Last annotation update)

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